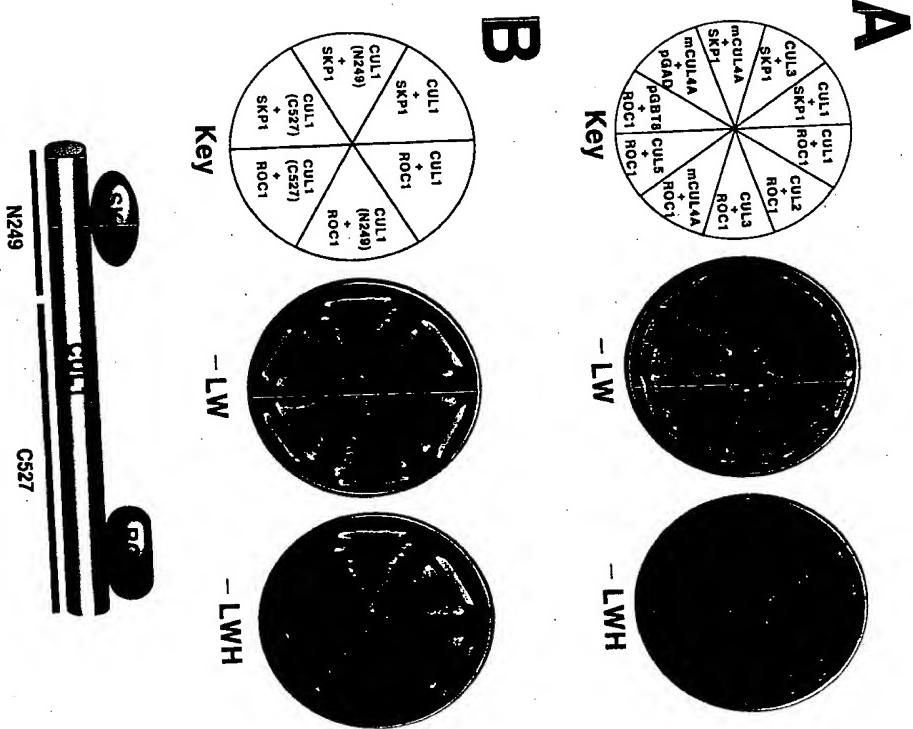


FIGURE 1



A. ROC1

**A.** *ROC1*

ATGCCGGCCAGCGATGGATGCTGATACCCGAGCGGCCAACAGGGCGGAAAGAGCCTTGAGTGAAGAAAAGTGGATGCGATA M A A M D V D T P S G T N S G A G K K R F E V K K W N A V	1800	90
GCCCTCTGGCCCTGGATATTGTGTTGATACTGTGCACACTGAGCATTTTCATAGAMTGTCAAGCTTACAG A L W A W D I V V D N C A I C R N H I M D L C I E C Q A N Q	60	30
GGCTCCGCTTACTCAGAGCTTACTGTGCGAGGGAGCTTGTAACCAGATGCTTTCACTCCACTGCACTCTCGTGGCTCAAACA A S A T S E C T V A W G V C N H A F H F H C I S R W L K T	270	90
CGACAGGTTGTCATGGACACAGAGAGTGGCAATTCCANAGTATGGCACTAG 327 R Q V C P L D N R E W E F Q K Y G H * 108	30	30

B.  
ROC2

**B.** **ROC2**

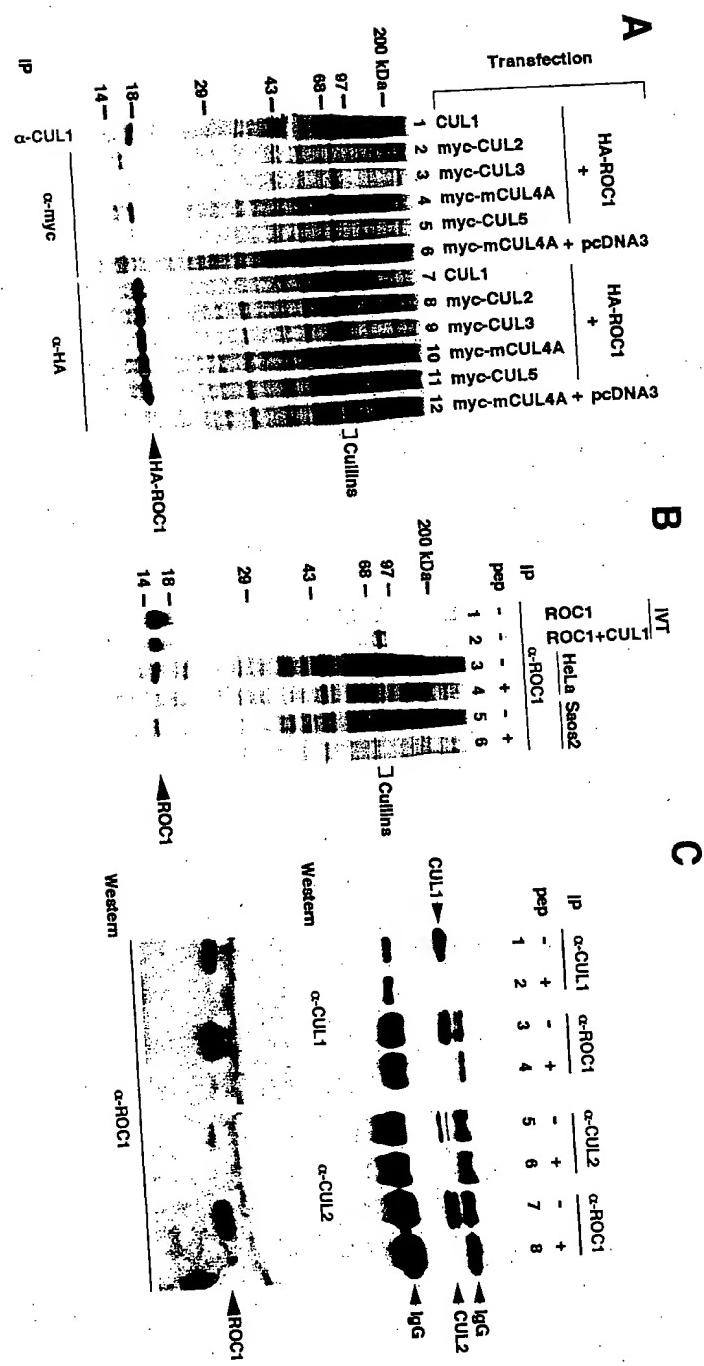
ATGCCCGACGGAGAAGGAAACCTGGCCCTGGCTCTCACTCCGGAGCTAACGTCAGCTCAAGCTGGGAGGGCAGAACAGATGTC	90
M A D V E D G E E P C V L S S H S G S A G S K S G G D K M F	186
TCCCTCTAGAAGTGGACCCGGGGAGCATGTGGACTCTGGGAGCTGGGACTGGGACTGGCATGCGCCATCTGCAGGGCCASGGTGATGGATGCC	187
S L K K W N A V A M W S W D V E C D T C A I C R V Q V M D A	188
TGTCCTAGAGTCAAGCTGAAACAAACAGAGGACTGTGTTGGCTGGGAGAGTGTAAATCTCCACACTGTCATGTC	27
C L R C Q A E N K Q E D C V V V W G E C N H S F H N C C M S	9
CTCTGGGTGAAACAGAACAAATCGCTGCCCTCTGGCAGGGAGCTGGGAGTCCAAAGATCGGCCAAATGA	342
L W V K Q N N R C P L C Q Q D W V V Q R I G K *	113

१

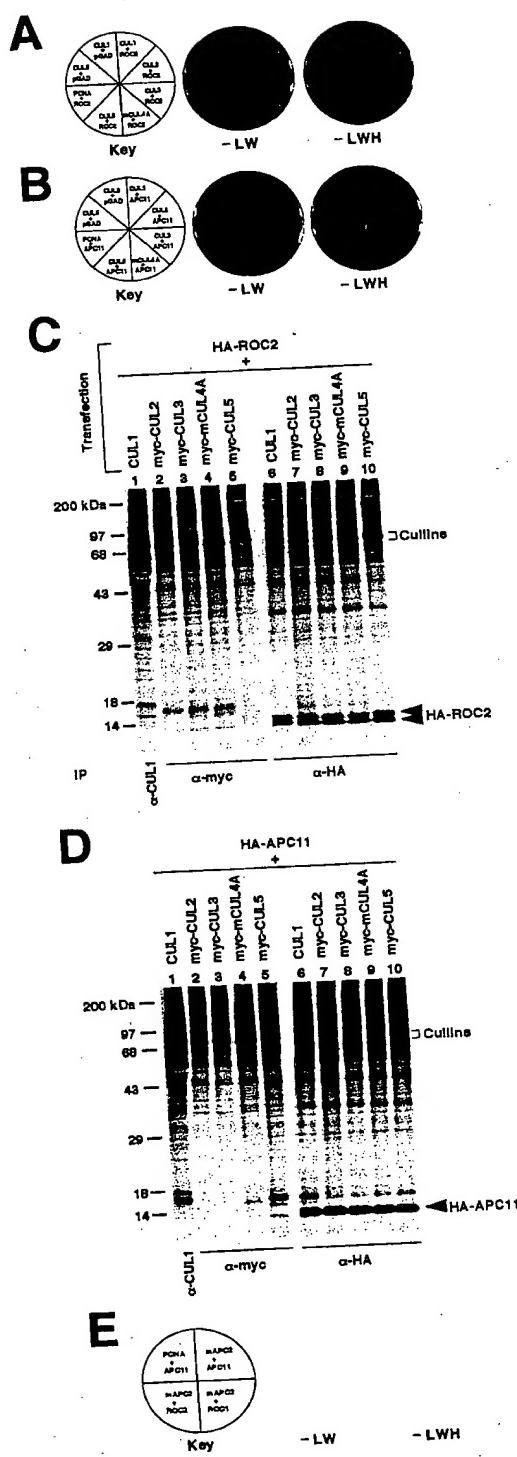
		C.
ROC1-Hs	22	FEVKKNAVALWAWDIDVVDNCALCRNHIMDICIECOANOASATSEECTVAVGVNHAFFHCTISWML--KTRQVCPIDNRREWEF
ROC1-Dm	22	FEVKKNAVALWAWDIDVVDNCALCRNHIMDICIECOANOASATSEECTVAVGVNHAFFHCTISWML--KTRQVCPIDNRREWEF
ROC1-Ce	24	FEVKKNAVALWAWDIDVVDNCALCRNHIMDICIECOANOASATSEECTVAVGVNHAFFHCTISWML--KTRQVCPIDNRREWEF
ROC1-At	32	FEIKKNAVALWAWDIDVVDNCALCRNHIMDICIECOANOASATSEECTVAVGVNHAFFHCTISWML--NTRAVCPIDNRREWEF
ROC1-SP	21	FEIKKNAVALWAWDIDVVDNCALCRNHIMDICIECOANOASATSEECTVAVGVNHAFFHCTISWML--KTRDACPDLNQPWQL
ROC1-SC	35	FEIKKNAVALWAWDIDVVDNCALCRNHIMDICIECOANOASATSEECTVAVGVNHAFFHCTISWML--KONRCPLCQODWWV
ROC2-Hs	2	FSLKKKNAVAMWSWDVECDTCATGRVQMDACIRCOAEN---KQEDCVVVGCGNHSFRCCMSLWV--RQNRRCPICQODWWV
ROC2-Ce	30	FVLKKWNALAWWADVECDTCATGRVHMEECURCQSEP---SAB-CYVWGDGNSFHICCMQIWI--
APC11-Hs	3	VKIKCWNGVATWLVVANDENGCGICRMAGFNGCPCDKVPG----DDCP1MWGVESHCFAHVCMVCTWLNQPLNKQCPMCROSWE
APC11-Dm	3	VTKKSWIGVATWWRWLANDENGCGICRMAGFNGCPCDKVPG----DDCP1MWGVESHCFAHVCMVCTWLNQPLNKQCPMCROSWE
APC11-Ce	51	ITWKKLHVCGWIKWL [3] DTGCGICRMAGFESACNNCKFPG----DQCP1VIGLCHENPHDHC1YRWLDTPISKGLCPMCROTFOI
APC11-SC	3	VKIKEWHSVFAWSW [21] DV <u>GICRAS</u> YNGTCPBCKFPG----

FIG. 2

**FIGURE 3**



**FIGURE 4**



0.05% Galactose

## FIGURE 5

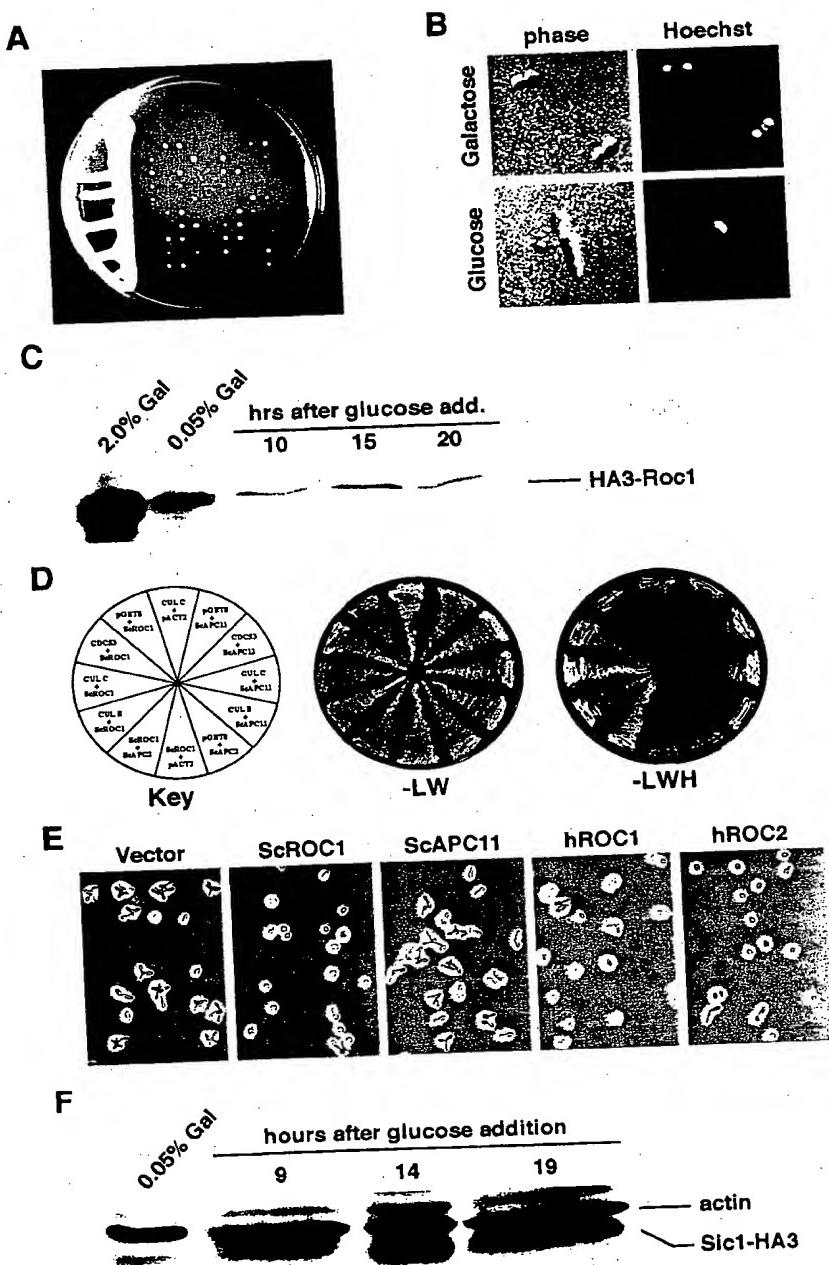


FIGURE 6

